

SEQUENCE LISTING

<110> Mendel Biotechnology, Inc.
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<120> PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS

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 <151> 2002-06-14

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<150> 60/336,049
<151> 2001-11-19

<150> Polynucleotides and Polypeptides in Plants
<151> 2003-09-18

<150> 60/434,166
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Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp
35 40 45

Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
50 55 60

Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val
65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
85 90 95

Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
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          20          25          30

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Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn
          35          40          45

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Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Met Gln Glu Cys Val Ser
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Glu Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys
65          70          75          80

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Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr
          85          90          95

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Thr Leu Gly Phe Glu Asp Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln
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Arg Phe Arg Glu Ile Glu Gly Glu Arg Thr Gly Leu Gly Arg Pro Gln
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Thr Gly Gly Glu Val Gly Glu His Gln Arg Asp Ala Val Gly Asp Gly
130 135 140

Gly Gly Phe Tyr Gly Gly Gly Gly Gly Met Gln Tyr His Gln His His
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Gln Phe Leu His Gln Gln Asn His Met Tyr Gly Ala Thr Gly Gly Gly
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<223> G485

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ataagtttca tcaccggtga ggcttctgac aagtgtcaga gagagaagag gaagacaatc 240
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20 25 30

Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp
35 40 45

Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
50 55 60

Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile
65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp
85 90 95

Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Val Glu
100 105 110

Gly Glu Lys Thr Thr Thr Ala Gly Arg Gln Gly Asp Lys Glu Gly Gly
115 120 125

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130 135 140

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Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Arg Gly Leu
35 40 45

Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Ile Val Gln Glu
50 55 60

Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys
65 70 75 80

Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp
85 90 95

Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Met Glu Pro Leu Lys Val
100 105 110

Tyr Leu Met Arg Tyr Arg Glu Gly Asp Thr Lys Gly Ser Ala Lys Gly
115 120 125

Gly Asp Pro Asn Ala Lys Lys Asp Gly Gln Ser Ser Gln Asn Gly Gln
130 135 140

Phe Ser Gln Leu Ala His Gln Gly Pro Tyr Gly Asn Ser Gln Val Thr
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Phe Pro Leu Phe Ser Ser His Ser Ser Asn Thr His His Ser Leu Leu
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Ile Cys

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			20					25					30		
Phe	Leu	Pro	Ile	Ala	Asn	Ile	Ser	Arg	Ile	Met	Lys	Arg	Gly	Leu	Pro
			35				40					45			
Leu	Asn	Gly	Lys	Ile	Ala	Lys	Asp	Ala	Lys	Glu	Thr	Met	Gln	Glu	Cys
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Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Asp Pro Leu Lys Val Tyr
100 105 110

Leu Met Arg Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Gly Lys
115 120 125

Gly Gly Glu Ser Ser Ala Lys Arg Asp Gly Gln Pro Ser Gln Val Ser
130 135 140

Gln Phe Ser Gln Val Pro Gln Gln Gly Ser Phe Ser Gln Gly Pro Tyr
145 150 155 160

Gly Asn Ser Gln Ser Leu Arg Phe Gly Asn Ser Ile Glu His Leu Glu
165 170 175

Val Leu Met Ser Ser Thr Arg Thr Leu Phe Ile Thr Ile Phe Arg Asp
180 185 190

Ser Thr Met Pro Val Val Ser Glu Asn Leu Ser Asp Pro Leu Ser Ile
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Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Gly
 35 40 45

Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
 50 55 60

Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu
 65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr
 85 90 95

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Leu Gly Phe Glu Asp Tyr Met Asp Pro Leu Lys Ile Tyr Leu Thr Arg
100 105 110

Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Ala Lys Gly Gly Asp
115 120 125

Ser Ser Ala Lys Arg Asp Val Gln Pro Ser Pro Asn Ala Gln Leu Ala
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Arg His Met Met Val Pro Met Gln Gly Pro Glu
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Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu
 35 40 45

Pro Pro Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu
 50 55 60

Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys
 65 70 75 80

Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp
 85 90 95

Ala Met Thr Thr Leu Gly Phe Glu Glu Tyr Ile Asp Pro Leu Lys Val
 100 105 110

Tyr Leu Ala Ala Tyr Arg Glu Ile Glu Gly Asp Ser Lys Gly Ser Ala
 115 120 125

Lys Gly Gly Asp Ala Ser Ala Lys Arg Asp Val Tyr Gln Ser Pro Asn
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Gly Gln Val Ala His Gln Gly Ser Phe Ser Gln Gly Val Asn Tyr Thr
 145 150 155 160

Asn Ser

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20          25          30

Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala
35          40          45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
50          55          60

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Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu
65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr
85 90 95

Leu Gly Phe Glu Asp Tyr Val Asp Pro Leu Lys Ile Tyr Leu His Lys
100 105 110

Tyr Arg Glu Met Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His
115 120 125

Glu Arg Asp Glu Gly Tyr Gly His Gly His Gly His Ala Thr Pro Met
130 135 140

Met Thr Met Met Met Gly His Gln Pro Gln His Gln His Gln His Gln
145 150 155 160

His Gln His Gln His Gln Gly His Val Tyr Gly Ser Gly Ser Ala Ser
165 170 175

Ser Ala Arg Thr Arg
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<223> G3476 GLYMA-28NOV01-CLUSTER33504_3

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ttctcccat agcgaacgtg agcaggatca tgaagaaggc cttgccggcg aacgcgaaga 180
tctcgaagga cgcgaaggag acggtgcagg aatgcgtgtc ggagttcatc agcttcataa 240
cgggtgaggc gtcggacaag tgccagaggg agaagcgcaa gaccatcaac ggcgacgac 300
ttctctgggc catgacaacc ctgggattcg aagagtacgt ggagcctctg aagatttacc 360
tccagcgctt ccgcgagatg gagggagaga agaccgtggc cgcccgcgac tcttctaagg 420

MBI-0022CIP.ST25.txt

actcggcctc cgcctcctcc tatcatcagg gacacgtgta cggctcccct gcctaccatc 480
atcaagtgcc tgggcccact taccctgccc ctggtagacc cagatgacgt gctcctctat 540
tcgccactcc ctagactttn tatattatat tatttaatta aactctcttc tccactcaac 600
ctttgcaaga tcaactgggtt 620

<210> 18
<211> 165
<212> PRT
<213> Glycine max

<200>
<223> G3476 GLYMA-28NOV01-CLUSTER33504_3 polypeptide
<400> 18

Met Ala Glu Ser Asp Asn Asp Ser Gly Gly Ala Gln Asn Ala Gly Asn
1 5 10 15

Ser Gly Asn Leu Ser Glu Leu Ser Pro Arg Glu Gln Asp Arg Phe Leu
20 25 30

Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn
35 40 45

Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser
50 55 60

Glu Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg
65 70 75 80

Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr
85 90 95

Thr Leu Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Ile Tyr Leu Gln
100 105 110

Arg Phe Arg Glu Met Glu Gly Glu Lys Thr Val Ala Ala Arg Asp Ser
115 120 125

Ser Lys Asp Ser Ala Ser Ala Ser Ser Tyr His Gln Gly His Val Tyr
130 135 140

Gly Ser Pro Ala Tyr His His Gln Val Pro Gly Pro Thr Tyr Pro Ala
145 150 155 160

Pro Gly Arg Pro Arg
165

<210> 19
 <211> 1872
 <212> DNA
 <213> Glycine max

<200>
 <223> G3475 GLYMA-28NOV01-CLUSTER33504_5

<400> 19
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 ttctccttat atttattaaa ctataatata gtatatataa agaaaagatt ttgagaattt 180
 gaataaaata agagtgtcca agtcagaggc gagcacgtgc cagataccaa agcaacggtc 240
 cagatcatgg agcactcacc aaatccaagg gctcctatgt gtccgtgcaa actcacactt 300
 atcgcccaac aacgggtccac aaagcgccac gtgtttctca gataaagcgt tattaaccct 360
 tctgatccaa cggatcctgc tcattacctc ccaaacaagc ccttccgttc cgtttcacct 420
 ttctctttcc cgccggagcc gccgtcacc gccgcggca atcgatatcag accctcccaa 480
 tacaccgtct ccgacttcca cgcagaattg cagcattcat tgatttcaat tttcaagtct 540
 tgaggatttc gtttcaacag cgcttcaatt tgacgcagaa aaactgagtc aaaccaattc 600
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 ccgaagaaaa ctgcaccgaa cactgaatct cagttaccga ggagcttctt ctacgaaccg 720
 tgcttaattc cacacagaaa caccgagtca aactgggttc tgctgtgttc gtgggttcaga 780
 ttctcaatcg aaatttgaaa ttcagaagaa aaccgcaccg aacacagaat ttcagaatct 840
 gaacaagttt cttccgttaa cagcacttca acttcacgtg gaacaagaat caaacggtt 900
 cgtgggttcg attctcaatt cctcgtccat tcgcaatcga ttttcaaatt ccgaagaaaa 960
 ccgctccgaa cactgaattt cagactctga acagcgaaca gtacttcaag ttcacgtgga 1020
 acgagtcaaa gcgattccaa tcaatttcgc gaactcctcc acggtgaact ccgatatttt 1080
 cctgcactga cttagtgatt cgtttcatat ttctcagctt cgattatccg tttgtcgatg 1140
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 ccgcgggagc aggaccggtt cctgccgatc gcgaacgtga gccgcatcat gaagaaggcg 1260
 ctgccggcga acgcgaagat ctccaaggac gcgaaggaga cgggtgcagga gtgcgtgtcg 1320
 gagttcatca gtttcatcac cggcgaggcc tccgacaagt gccagcggga gaagcgcaag 1380
 acgatcaacg gcgacgacct gctctgggcg atgaccactc tcggcttcga ggactacgtc 1440
 gagcctctca agggctacct ccagcgcttc cgagaaatgg aaggagagaa gaccgtggcg 1500
 gcgcgtgaca aggacgcgcc tcctcctacc aatgctacca acagtgccta cgagagtcct 1560

MBI-0022CIP.ST25.txt

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tccaatgccg gtaggccag gtagatgggc ctatgttatt attattatta ttattcttat 1740
tcgtaagtta aaagaaatgt gagattcaaa gtggtgatta agtgaattag taacaaaaaa 1800
gtgcgactca gttgattaaa aatatatata aattattata agtcttttaa tatgtttttg 1860
attctcacac at 1872

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<210> . 20
<211> 188
<212> PRT
<213> Glycine max

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<200>
<223> G3475 GLYMA-28NOV01-CLUSTER33504_5 polypeptide
<400> 20

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Met Ala Asp Ser Asp Asn Asp Ser Gly Gly Ala His Asn Ala Gly Lys
1          5          10          15

Gly Ser Glu Met Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala
          20          25          30

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
          35          40          45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
          50          55          60

Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg
65          70          75          80

Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly
          85          90          95

Phe Glu Asp Tyr Val Glu Pro Leu Lys Gly Tyr Leu Gln Arg Phe Arg
          100          105          110

Glu Met Glu Gly Glu Lys Thr Val Ala Ala Arg Asp Lys Asp Ala Pro
          115          120          125

Pro Pro Thr Asn Ala Thr Asn Ser Ala Tyr Glu Ser Pro Ser Tyr Ala
          130          135          140

Ala Ala Pro Gly Gly Ile Met Met His Gln Gly His Val Tyr Gly Ser
145          150          155          160

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Ala Gly Phe His Gln Val Ala Gly Gly Ala Ile Lys Gly Gly Pro Val
165 170 175

Tyr Pro Gly Pro Gly Ser Asn Ala Gly Arg Pro Arg
180 185

<210> 21
<211> 521
<212> DNA
<213> Glycine max

<200>
<223> GLYMA-28NOV01-CLUSTER33504_6

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gacaacgagt ccggagggtca cacggggaac gcaagcggaa gcaacgaatt ctccggttgc 120
agggagcaag acagggttcct tccgatagcg aacgtgagca ggatcatgaa gaaggcggtg 180
ccggcgaaac cgaagatctc gaaggaggcg aaggagacgg tgcaggagtg cgtgtcggag 240
ttcatcagct tcataacagg agaagcgctc gataagtgcc agaaggagaa gaggaagacg 300
atcaacggcg atgatctgct gtgggccatg accacgctgg ggttcgagga gtacgtggag 360
cctctcaagg tttatctgca taagtatagg gagctggaag gggagaaaac tgctatgatg 420
ggaaggccac atgagagggg tgaggggttat ggtcatgcaa ctccatgat gatcatgatg 480
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<210> 22
<211> 158
<212> PRT
<213> Glycine max

<220>
<221> misc_feature
<222> (158)..(158)
<223> Xaa can be any naturally occurring amino acid

<200>
<223> GLYMA-28NOV01-CLUSTER33504_6 polypeptide

<400> 22

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1 5 10 15

Gly Ser Asn Glu Phe Ser Gly Cys Arg Glu Gln Asp Arg Phe Leu Pro
20 25 30

MBI-0022CIP.ST25.txt

Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala
35 40 45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
50 55 60

Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu
65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr
85 90 95

Leu Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Val Tyr Leu His Lys
100 105 110

Tyr Arg Glu Leu Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His
115 120 125

Glu Arg Asp Glu Gly Tyr Gly His Ala Thr Pro Met Met Ile Met Met
130 135 140

Gly His Gln Gln Gln Gln His Gln Gly His Val Tyr Gly Xaa
145 150 155

<210> 23
<211> 556
<212> DNA
<213> Glycine max

<200>
<223> G3471 GLYMA-28NOV01-CLUSTER4778_1

<400> 23
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acatcagccg cattatgaag aaggctctgc ctcccaacgg caagattgca aaggatgcca 180
aagacacccat gcaggaatgc gtttctgagt tcatcagctt cattaccagc gaggcgagtg 240
agaaatgccga gaaggagaag agaaagacaa tcaatggaga cgatttgcta tgggccatgg 300
ccacttttagg atttgaagac tacatagagc cgcttaaggt gtacctggct aggtacagag 360
aggcggaggg tgacactaaa ggatctgcta gaagtgggtga tggatctgct acaccagatc 420
aagttggcct tgcaggtcaa aattctcagc ttgttcatca gggttcgctg aactatattg 480
gtttgcaggt gcaaccacaa catctgggta tgccttcaat gcaaagccat gaatagttta 540
gatgcttcta cgcac 556

<210> 24
 <211> 173
 <212> PRT
 <213> Glycine max

<200>
 <223> G3471 GLYMA-28NOV01-CLUSTER4778_1 polypeptide

<400> 24

Met Ser Asp Ala Pro Pro Ser Pro Thr His Glu Ser Gly Gly Glu Gln
 1 5 10 15

Ser Pro Arg Gly Ser Ser Ser Gly Ala Arg Glu Gln Asp Arg Tyr Leu
 20 25 30

Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro Asn
 35 40 45

Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val Ser
 50 55 60

Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln Lys
 65 70 75 80

Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala
 85 90 95

Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Ala
 100 105 110

Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser Gly
 115 120 125

Asp Gly Ser Ala Thr Pro Asp Gln Val Gly Leu Ala Gly Gln Asn Ser
 130 135 140

Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val Gln
 145 150 155 160

Pro Gln His Leu Val Met Pro Ser Met Gln Ser His Glu
 165 170

<210> 25
 <211> 939
 <212> DNA
 <213> Glycine max

<220>
 <221> misc_feature

<222> (596)..(596)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (762)..(762)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (767)..(767)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (769)..(769)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (775)..(775)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (786)..(786)
<223> n is a, c, g, or t

<200>
<223> G3470 GLYMA-28NOV01-CLUSTER4778_3

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ctctttgtca ccgggtttgt gagatgtcgg atgcaccggc gagtccgagt cacgagagtg 180
gtggcgagca gagccctcgc ggctcgttgt ccggcgcggc tagagagcag gaccggtacc 240
ttcccattgc caacatcagc cgcacatga agaaggctct gcctcccaat ggcaagattg 300
cgaaggatgc aaaagacaca atgcaagaat gcgtttctga attcatcagc ttcattacca 360
gcgaggcgag tgagaaatgc cagaaggaga agagaaagac aatcaatgga gacgatttac 420
tatgggccat ggcaacttta gggtttgaag actacattga gccgcttaag gtgtacctgg 480
ctaggtacag agaggcgag ggtgacacta aaggatctgc tagaagtggg gatggatctg 540
ctagaccaga tcaagtggc cttgcaggtc aaaatgctca ggtgcaacca caacantctg 600
gttatgcctt caatgcaagg ccatgaatag tttagatgct tctacgcac ttatttattt 660
cccttgaatg cttgtacgca tggcatgggt ggaaccaatt gtctggtaaa aaaatggggg 720
ggctctcgtc ccccggggtg ggggggtttt gtttcggtac tngtgtngt tttnttaaa 780
acacgncttg tagcgggtgt ttctcttctc aaggagaga tgtgtttagg gttatgctag 840
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attatataag agagaatatt tgcagacaaa aagacttac

939

<210> 26
<211> 160
<212> PRT
<213> Glycine max

<220>
<221> misc_feature
<222> (151)..(151)
<223> Xaa can be any naturally occurring amino acid

<200>
<223> G3470 GLYMA-28NOV01-CLUSTER4778_3 polypeptide

<400> 26

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Ser Pro Arg Gly Ser Leu Ser Gly Ala Ala Arg Glu Gln Asp Arg Tyr
20 25 30

Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro
35 40 45

Asn Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val
50 55 60

Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln
65 70 75 80

Lys Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met
85 90 95

Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu
100 105 110

Ala Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser
115 120 125

Gly Asp Gly Ser Ala Arg Pro Asp Gln Val Gly Leu Ala Gly Gln Asn
130 135 140

Ala Gln Val Gln Pro Gln Xaa Ser Gly Tyr Ala Phe Asn Ala Arg Pro
145 150 155 160

<210> 27
<211> 1231
<212> DNA

<213> Oryza sativa

<200>

<223> ORYSA-22JAN02-CLUSTER26105_1

<400> 27

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tatgcctccc aatacagatt atatggaacc gaatgacagc caaagaccaa ttgttaaatt      180
atcctgaata tacatacaac aacagagcta gaccacgaac cgaaactatc ctcacgggga      240
gtaatttaca tctgagaagc agccttggct cgacgcttcc aagcagcatc agttcctggt      300
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tccatgagaa ccaagtacat cctttttcac agagccatca ccagcctttg cagttaattt      600
actatcacc cccatctctc tgtacttctg caggtagacc ttgaggggct cgatgtagtc      660
ctcgaagccc agcgtggcca tcgcccacag caagtcgctc ccgttgatgg tcttgcgctt      720
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ctcctgcacg gtctccttgg cgtccttggc gatcttcccg ttggccggga tggccttctt      840
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cccaccccc cctccccctc ctccccctcc cccccctggg ctcccgtctt cgtggctccc      960
ccctcctccc cccgggctcc ccggcccatc cgccatccca cctccccctt ccttatatag     1020
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gaggtggtga agcgaggagg agagagagag agagagagag agagagaggg ggggggagag     1140
gagagagaga ggaagcgggg gtgggaagcg gagcggaggt gaggcggaga ggcgagaggg     1200
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<210> 28

<211> 185

<212> PRT

<213> Oryza sativa

<200>

<223> ORYSA-22JAN02-CLUSTER26105_1 polypeptide

<400> 28

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1           5           10          15

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MBI-0022CIP.ST25.txt

Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30

Gly Gly Pro Leu Val Arg Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile
35 40 45

Ser Arg Ile Met Lys Lys Ala Ile Pro Ala Asn Gly Lys Ile Ala Lys
50 55 60

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
65 70 75 80

Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
85 90 95

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu
100 105 110

Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met
115 120 125

Glu Gly Asp Ser Lys Leu Thr Ala Lys Ala Gly Asp Gly Ser Val Lys
130 135 140

Lys Asp Val Leu Gly Ser His Gly Gly Ser Ser Ser Ser Ala Gln Gly
145 150 155 160

Met Gly Gln Gln Ala Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro
165 170 175

Gln Tyr His Asn Gly Asp Val Ser Asn
180 185

<210> 29
<211> 229
<212> PRT
<213> Oryza sativa

<200>
<223> OSC12630.C1.p5.fg polypeptide

<400> 29

Met Pro Asp Ser Asp Asn Glu Ser Gly Gly Pro Ser Asn Ala Gly Glu
1 5 10 15

Tyr Ala Ser Ala Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val
20 25 30

MBI-0022CIP.ST25.txt

Ser Arg Ile Met Lys Arg Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys
35 40 45

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
50 55 60

Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
65 70 75 80

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu
85 90 95

Asp Tyr Ile Asp Pro Leu Lys Leu Tyr Leu His Lys Phe Arg Glu Leu
100 105 110

Glu Gly Glu Lys Ala Ile Gly Ala Ala Gly Ser Gly Gly Gly Gly Ala
115 120 125

Ala Ser Ser Gly Gly Ser Gly Ser Gly Ser Gly Ser His His His Gln
130 135 140

Asp Ala Ser Arg Asn Asn Gly Gly Tyr Gly Met Tyr Gly Gly Gly Gly
145 150 155 160

Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Ser Pro Pro Ala
165 170 175

Ser Ser Ala Gly Tyr Ala Gln Pro Gln Pro Pro His His His His His
180 185 190

Gln Met Val Met Gly Gly Lys Gly Lys Val Glu Glu Val Gln Ser Lys
195 200 205

Gly Lys Ile Arg Asp Phe Leu Gln Leu Gln Ala Ser Met Leu Glu Leu
210 215 220

Ile Gln Gly Glu Asn
225

<210> 30
<211> 241
<212> PRT
<213> Oryza sativa

<200>
<223> OSC1404.C1.p3.fg polypeptide

<400> 30

MBI-0022CIP.ST25.txt

Met Ser Glu Gly Phe Asp Gly Thr Glu Asn Gly Gly Gly Gly Gly Gly
 1 5 10 15

Gly Gly Val Gly Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile
 20 25 30

Gly Arg Ile Met Arg Arg Ala Val Pro Glu Asn Gly Lys Ile Ala Lys
 35 40 45

Asp Ser Lys Glu Ser Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
 50 55 60

Ile Thr Ser Glu Ala Ser Asp Lys Cys Leu Lys Glu Lys Arg Lys Thr
 65 70 75 80

Ile Asn Gly Asp Asp Leu Ile Trp Ser Met Gly Thr Leu Gly Phe Glu
 85 90 95

Asp Tyr Val Glu Pro Leu Lys Leu Tyr Leu Arg Leu Tyr Arg Glu Gly
 100 105 110

Asp Thr Lys Gly Ser Arg Ala Ser Glu Leu Pro Val Lys Lys Asp Val
 115 120 125

Val Leu Asn Gly Asp Pro Gly Ser Ser Leu Val Asn Tyr Gly Ala Gln
 130 135 140

Arg Ala Asp Ala Asn Ala Asn His Leu Asp Leu Phe Phe Leu Leu Arg
 145 150 155 160

Lys Asn Pro Glu Ser Thr Thr Ala Asn Cys Met Arg Glu Asp Glu Ala
 165 170 175

Lys Pro Val Thr Val Lys Ile Ile Glu Thr Val Tyr Val Glu Ala Asp
 180 185 190

Thr Ala Asp Asp Phe Lys Ser Val Val Gln Arg Leu Thr Gly Lys Asp
 195 200 205

Ala Val Ala Gly Asp Ala Pro Glu Leu Asn Ser Ala Gln Arg Phe Gly
 210 215 220

Ser Gly Arg Glu Ala Ser Arg His Gly Asp His Lys Val Arg Ile Tyr
 225 230 235 240

Glu

<210> 31
 <211> 297
 <212> PRT
 <213> Oryza sativa

<200>
 <223> OSC30077.C1.p6.fg polypeptide
 <400> 31

Met Lys Ser Arg Lys Ser Tyr Gly His Leu Leu Ser Pro Val Gly Ser
 1 5 10 15

Pro Pro Leu Asp Asn Glu Ser Gly Glu Ala Ala Ala Ala Ala Ala Ala
 20 25 30

Gly Gly Gly Gly Cys Gly Ser Ser Ala Gly Tyr Val Val Tyr Gly Gly
 35 40 45

Gly Gly Gly Gly Asp Ser Pro Ala Lys Glu Gln Asp Arg Phe Leu Pro
 50 55 60

Ile Ala Asn Val Ser Arg Ile Met Lys Arg Ser Leu Pro Ala Asn Ala
 65 70 75 80

Lys Ile Ser Lys Glu Ser Lys Glu Thr Val Gln Glu Cys Val Ser Glu
 85 90 95

Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu
 100 105 110

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr
 115 120 125

Leu Gly Phe Glu Ala Tyr Val Gly Pro Leu Lys Ser Tyr Leu Asn Arg
 130 135 140

Tyr Arg Glu Ala Glu Gly Glu Lys Ala Asp Val Leu Gly Gly Ala Gly
 145 150 155 160

Gly Ala Ala Ala Ala Arg His Gly Glu Gly Gly Cys Cys Gly Gly Gly
 165 170 175

Gly Gly Gly Ala Asp Gly Val Val Ile Asp Gly His Tyr Pro Leu Ala
 180 185 190

Gly Gly Leu Ser His Ser His His Gly His Gln Gln Gln Asp Gly Gly

195 200 205

Gly Asp Val Gly Leu Met Met Gly Gly Gly Asp Ala Gly Val Gly Tyr
210 215 220

Asn Ala Gly Ala Gly Ser Thr Thr Thr Ala Phe Tyr Ala Pro Ala Ala
225 230 235 240

Thr Ala Ala Ser Gly Asn Lys Ala Tyr Cys Gly Gly Asp Gly Ser Arg
245 250 255

Val Met Glu Phe Glu Gly Ile Gly Gly Glu Glu Glu Ser Gly Gly Gly
260 265 270

Gly Gly Gly Gly Glu Arg Gly Phe Ala Gly His Leu His Gly Val Gln
275 280 285

Trp Phe Arg Leu Lys Arg Asn Thr Asn
290 295

<210> 32
<211> 285
<212> PRT
<213> Oryza sativa

<200>
<223> OSC5489.C1.p2.fg polypeptide

<400> 32

Met Ala Asp Ala Gly His Asp Glu Ser Gly Ser Pro Pro Arg Ser Gly
1 5 10 15

Gly Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg
20 25 30

Ile Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala
35 40 45

Lys Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr
50 55 60

Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn
65 70 75 80

Gly Glu Asp Leu Leu Phe Ala Met Gly Thr Leu Gly Phe Glu Glu Tyr
85 90 95

Val Asp Pro Leu Lys Ile Tyr Leu His Lys Tyr Arg Glu Met Glu Gly

100		105		110
Asp Ser Lys Leu Ser Ser Lys Ala Gly Asp Gly Ser Val Lys Lys Asp				
115		120		125
Thr Ile Gly Pro His Ser Gly Ala Ser Ser Ser Ser Ala Gln Gly Met				
130		135		140
Val Gly Ala Tyr Thr Gln Gly Met Gly Tyr Met Gln Pro Gln Ser Asn				
145		150		155
Phe His Ile Leu Val Val Leu Gln Ser Phe Ala Phe Pro Tyr Met Tyr				
	165		170	175
Gln Val Ala Gln Ile Tyr Cys Asn Lys Tyr Glu Val Ser Arg Glu Gln				
	180		185	190
Ile Trp Asp Thr Pro Gln Ile Met Glu Leu Ser Pro Trp Ile Pro Tyr				
	195		200	205
Thr Ile Asn Arg Ile Trp Lys Glu Thr His Gly Ser Gln Asp Ile Arg				
	210		215	220
Ile Gln Gly Arg Pro Arg Glu Ala Ala Asn Ser Ala Leu Asp Trp Gln				
225		230		235
Trp Pro Ser Lys His Ser Ser Leu Ala Ser Asn Phe Tyr Gly Thr Arg				
	245		250	255
Val Val Gly Gly His His Glu Tyr Gln Arg Ser Thr Lys Lys Asp Thr				
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	275		280	285

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 <213> Zea mays

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cgtgggggtac tgcggcggcg gcggcggtga gtcgccggcc aaggagcaag accggttcct	180

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ggaggcctcc gacaagtgcc agcgcgagaa gcgcaagacc atcaacggcg acgacctgct 360
ctggggccatg accacgctcg gcttcgaggc ctacgtcgcc ccactcaagt cctacctcaa 420
ccgctaccgc gaggccgagg gcgagaaggc cgccgtgcta ggcggcggcg cgcgccacgg 480
cgacggcggc ggcgcggcgg acgacgccgg ccactcgcc ggg 523

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 <212> PRT
 <213> Zea mays

<200>
 <223> LIB3732-044-Q6-K6-C4 polypeptide

<400> 34

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Val Gly Ser Pro Leu Ser Asp Asn Glu Ser Gly Ala Ala Ala Ala Ala
 20 25 30

Gly Gly Gly Gly Cys Gly Ser Ser Val Gly Tyr Cys Gly Gly Gly Gly
 35 40 45

Gly Glu Ser Pro Ala Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn
 50 55 60

Val Ser Arg Ile Met Lys Arg Ser Leu Pro Ala Asn Ala Lys Ile Ser
 65 70 75 80

Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser
 85 90 95

Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys
 100 105 110

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe
 115 120 125

Glu Ala Tyr Val Ala Pro Leu Lys Ser Tyr Leu Asn Arg Tyr Arg Glu
 130 135 140

Ala Glu Gly Glu Lys Ala Ala Val Leu Gly Gly Gly Ala Arg His Gly
 145 150 155 160

Asp Gly Gly Gly Ala Ala Asp Asp Ala Gly Pro Leu Ala Gly
165 170

<210> 35
<211> 1199
<212> DNA
<213> Zea mays

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gccactaata attttctctc tgtacgcact cagtaccaca atgggggaaac ctaataaagg 780
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<211> 166
<212> PRT
<213> Zea mays

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<400> 36

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Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile
20 25 30

Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys
35 40 45

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser
50 55 60

Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly
65 70 75 80

Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Val
85 90 95

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp
100 105 110

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala
115 120 125

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln
130 135 140

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Val Ile
145 150 155 160

Tyr Arg Thr Val Ile Cys
165

<210> 37

<211> 564

<212> DNA

<213> Zea mays

<200>

<223> ZEAMA-08NOV01-CLUSTER719_10

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cctccctcca cggtgctcgc gcccgctt atataagtgc acgaggagga gctcatggcg 180

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 ctaaggagac cgtgcaggag tgcgtctcgg agttcatctc cttcatcact agcgaggcga 420
 gtgacaagtg ccagaggag aagcggaaga ccatcaatgg cgacgacctg ctgtggggcca 480
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<210> 38
 <211> 188
 <212> PRT
 <213> Zea mays

<220>
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<200>
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<400> 38

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 1 5 10 15

Ala Leu Pro Ala Arg Ser Leu Arg His Leu Arg Pro Pro Pro Ala Leu
 20 25 30

Gly Arg Ser Pro Pro Ala Leu Pro Ser Leu His Val Ala Arg Ala Arg
 35 40 45

Ala Tyr Ile Ser Ala Arg Gly Gly Ala His Gly Gly Arg Ser Gly Glu
 50 55 60

Pro Trp Gly Arg Arg Arg Glu Pro His Ala Glu Arg Glu Pro Pro Gly
 65 70 75 80

Pro Ala Glu Val Glu Ala Val Ala Ala Val Arg Glu Gln Asp Arg Phe
 85 90 95

Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Ile Pro Ala
 100 105 110

Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val
 115 120 125

Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln
 130 135 140

Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met
 145 150 155 160

Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu
 165 170 175

Gln Lys Tyr Arg Glu Met Glu Gly Asp Ser Lys Xaa
 180 185

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 <213> Zea mays

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 agcaggaccg gttcctgccc atcgccaaca tcagccggat catgaagaag gccgtcccg 300
 ccaacggcaa gatcgccaag gacgctaagg agaccctgca ggagtgcgtc tccgagttca 360
 tatcattcgt gaccagcgag gccagcgaca aatgccagaa ggagaaacga aagacaatca 420
 acggggacga tttgctctgg gcgatggcca cttaggatt cgaggagtac gtcgagcctc 480
 tcaagattta cctacaaaag tacaaagaga tggaggggtga tagcaagctg tctacaaagg 540
 ctggcgaggg ctctgtaaag aaggatgcaa ttagtcccca tggcggcacc agtagctcaa 600
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 tctgcgatgg ctgcctctca ggtgtaaatt ggcttcgggt tagcgtgct tttgtccgta 840
 tatttaggat gatttgactg ttgctacttt tggcaacctt ttacatttac agatatgtat 900
 tattcagcat aaatataata tagtagtcct aggcctaaat aatgggtgatt aacataccaa 960
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 tgaatgtgat ggttgccctga atcctaattt gcc 1053

<210> 40
 <211> 164
 <212> PRT
 <213> Zea mays

<200>
 <223> ZEAMA-08NOV01-CLUSTER719_2 polypeptide

<400> 40

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Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile
 20 25 30

Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys
 35 40 45

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser
 50 55 60

Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly
 65 70 75 80

Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Val
 85 90 95

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp
 100 105 110

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala
 115 120 125

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln
 130 135 140

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His
 145 150 155 160

Asn Gly Glu Thr

<210> 41
 <211> 1178
 <212> DNA
 <213> Zea mays

<200>
 <223> ZEAMA-08NOV01-CLUSTER719_3

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gggaggcgga ggcggtggca gcgtcaggga gcaggacagg ttcctgcca tcgccaacat 300
cagtcgcatc atgaagaagg ccatcccggc taacgggaag accatcccgg ctaacgggaa 360
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cactagcgag gcgagtgaca agtgccagag ggagaagcgg aagaccatca atggcgacga 480
cctgctgtgg gccatggcca cgctgggggt tgaggactat attgaacccc tcaaggtgta 540
cctgcagaag tacagagaga tggaggggtga tagtaagtta acttcaaaat ccagcgatgg 600
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gggtcaacaa ggaacataca accaaggaat gggttatatg caaccccagt accataacgg 720
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<210> 42
<211> 185
<212> PRT
<213> Zea mays

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<200>
<223> ZEAMA-08NOV01-CLUSTER719_3 polypeptide

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<400> 42

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Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Gly Ser His Glu
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Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
20          25          30

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Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala

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35

40

45

Ile Pro Ala Asn Gly Lys Thr Ile Pro Ala Asn Gly Lys Ile Ala Lys
50 55 60

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
65 70 75 80

Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
85 90 95

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu
100 105 110

Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met
115 120 125

Glu Gly Asp Ser Lys Leu Thr Ser Lys Ser Ser Asp Gly Ser Ile Lys
130 135 140

Lys Asp Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Val Gln Gly
145 150 155 160

Met Gly Gln Gln Gly Thr Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro
165 170 175

Gln Tyr His Asn Gly Asp Ile Ser Asn
180 185

<210> 43
<211> 2109
<212> DNA
<213> Zea mays

<200>
<223> ZEAMA-08NOV01-CLUSTER719_4

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tcaggagca ggacaggttc ctgcccacg ccaacatcag tcgcatcatg aagaaggcca 240
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 <212> PRT

<213> Zea mays

<200>

<223> ZEAMA-08NOV01-CLUSTER719_4 polypeptide

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Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
35 40 45

Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln
50 55 60

Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp
65 70 75 80

Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu
85 90 95

Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys
100 105 110

Val Tyr Leu Gln Lys Tyr Arg Glu Val Arg Thr Val Phe Gly Asn Leu
115 120 125

Gly Val Arg Ser Cys Asn Arg Gln Ser Val Thr Trp Pro Ile Val Pro
130 135 140

Leu Ile Glu Leu Lys
145

<210> 45

<211> 1255

<212> DNA

<213> Zea mays

<200>

<223> ZEAMA-08NOV01-CLUSTER719_5

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ccctccctc cacttgctc gcacccgcgc ttatataagt gcaggaggag ctcatggcgg 180

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 <211> 178
 <212> PRT
 <213> Zea mays

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Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
 35 40 45

Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln
 50 55 60

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Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp
65 70 75 80

Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu
85 90 95

Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys
100 105 110

Val Tyr Leu Gln Lys Tyr Arg Glu Met Glu Gly Asp Ser Lys Leu Thr
115 120 125

Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp Ala Leu Gly His Val
130 135 140

Gly Ala Ser Ser Ser Ala Ala Gln Gly Met Gly Gln Gln Gly Ala Tyr
145 150 155 160

Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His Asn Gly Asp Ile
165 170 175

Ser Asn

<210> 47
<211> 1173
<212> DNA
<213> Zea mays

<200>
<223> G3435 ZEAMA-08NOV01-CLUSTER90408_1

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gactcgccaa atttccctcc ctctctctag ccttctcgtc gctcctgttc ttctcgcatc 180
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gatcatgaag aaggcgctcc cggccaacgc caagatcagc aaggacgcca aggagacggt 420
gcaggagtgc gtgtccgagt tcatctcctt catcaccggc gaggcctccg acaagtgcc 480
gcgcgagaag cgcaagacca tcaacggcga cgacctgctg tgggcatga ccacgctcgg 540
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MBI-0022CIP.ST25.txt

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cgcatgatg atgatgatga tggggcagcc catgtacggc ggctcgcagc cgcagcaaca      780
gccgccgag cctcagccgc cacagcagca gcagcagcaa catcaacagc atcacatggc      840
aatgggaggc agaggaggat tcggccaaca aggcggcggc ggtggctcct cgtcgtcgtc      900
agggcttggc cggcaagaca gggcgtgagt tgcgacgata cgttcagaat cagaatcgct      960
gatactcta cgtagaatta tacctaccta attgatgaca ccgcaccgca cctcgttgtg    1020
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<210> 48
 <211> 223
 <212> PRT
 <213> Zea mays

<200>
 <223> G3435 ZEAMA-08NOV01-CLUSTER90408_1 polypeptide

<400> 48

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Glu Leu Ser Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn
 20 25 30

Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser
 35 40 45

Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser
 50 55 60

Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys
 65 70 75 80

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe
 85 90 95

Glu Asp Tyr Val Glu Pro Leu Lys His Tyr Leu His Lys Phe Arg Glu
 100 105 110

Ile Glu Gly Glu Arg Ala Ala Ala Ser Ala Gly Ala Ser Gly Ser Gln
 115 120 125

MBI-0022CIP.ST25.txt

Gln Gln Gln Gln Gln Gly Glu Leu Pro Arg Gly Ala Ala Asn Ala Ala
130 135 140

Gly Tyr Ala Gly Tyr Gly Ala Pro Gly Ser Gly Gly Met Met Met Met
145 150 155 160

Met Met Gly Gln Pro Met Tyr Gly Gly Ser Gln Pro Gln Gln Gln Pro
165 170 175

Pro Gln Pro Gln Pro Pro Gln Gln Gln Gln Gln Gln His Gln Gln His
180 185 190

His Met Ala Met Gly Gly Arg Gly Gly Phe Gly Gln Gln Gly Gly Gly
195 200 205

Gly Gly Ser Ser Ser Ser Ser Gly Leu Gly Arg Gln Asp Arg Ala
210 215 220

<210> 49
<211> 1064
<212> DNA
<213> Zea mays

<200>
<223> G3436 ZEAMA-08NOV01-CLUSTER90408_2

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gttcggtggc tcggccgcga tgccggactc cgacaacgag tccggcgggc cgagcaacgc 180
ggagttctcg tcgccgcggg agcaggaccg gttcttgccg atcgcgaaacg tgagccggat 240
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ggagtgcgtg tccgagttca tctccttcat caccggcgag gcctccgaca agtgccagcg 360
cgagaagcgc aagaccatca acggcgacga cctgctctgg gccatgacca cgctcggett 420
cgaggactac gtcgagccgc tcaagctcta cctgcacaag ttccgcgagc tcgagggcga 480
gaaggcggcc acgacgagcg cctcctccgg ccgcgagccg ccgctgcaca gggagacgac 540
gccgtcgtcg tcaacgcaca atggcgcggg cgggcccgtc gggggatacg gcatgtacgg 600
cggcgcgggc gggggaagcg gtatgatcat gatgatgggg cagcccatgt acggcggctc 660
ccgcgccggc gcgtcgtccg ggtcgtaccc gcaccaccag atggccatgg gcggaaaagg 720
tggcgccctat ggctacggcg gaggctcgtc gtcgtcgccg tcagggctcg gcaggtagga 780
caggttggtga ccgtcgccgt ccatgcttgc atggccatgg ccatggctcg gctccccgcg 840

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 atggttaaga tagctccata acctctcggt aattaatcct gtgatttgta ctcccaagct 1020
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<210> 50
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 <213> Zea mays

<200>
 <223> G3436 ZEAMA-08NOV01-CLUSTER90408_2 polypeptide
 <400> 50

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 1 5 10 15

Ser Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Ser
 20 25 30

Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp
 35 40 45

Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
 50 55 60

Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile
 65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp
 85 90 95

Tyr Val Glu Pro Leu Lys Leu Tyr Leu His Lys Phe Arg Glu Leu Glu
 100 105 110

Gly Glu Lys Ala Ala Thr Thr Ser Ala Ser Ser Gly Pro Gln Pro Pro
 115 120 125

Leu His Arg Glu Thr Thr Pro Ser Ser Ser Thr His Asn Gly Ala Gly
 130 135 140

Gly Pro Val Gly Gly Tyr Gly Met Tyr Gly Gly Ala Gly Gly Gly Ser
 145 150 155 160

Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Gly Ser Pro Pro
 165 170 175

MBI-0022CIP.ST25.txt

Ala Ala Ser Ser Gly Ser Tyr Pro His His Gln Met Ala Met Gly Gly
180 185 190

Lys Gly Gly Ala Tyr Gly Tyr Gly Gly Gly Ser Ser Ser Ser Pro Ser
195 200 205

Gly Leu Gly Arg
210

<210> 51
<211> 1818
<212> DNA
<213> Glycine max

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<223> G3473 GLYMA-28NOV01-CLUSTER33504_4

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taagataaga gtgtccaggt cagaggcgag cacgtgccag ataccaaaagc aacgggtccag 240
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gactaacaac ggtccacaaa tcgccacgtg tcttcaagat aaagcggtat taacccttct 360
gatccaacgg atcctgctca ttatctccca aacaaacccc tccgttccgt ttcacctttc 420
cccttcccgc cggagccgcc gtcaccggct gctggccacc gtatccgacc ctccaatac 480
accctttccg agtcccacac aaaattgcac gattctgtga tttcaatttt caggtctcga 540
ggatttcggt tcagaagcgc ttccatttga cgcagaacca ccgactcaa ccgattcgcg 600
ccgagttcgt gactcgaatt ttcaacttct cattcatatt ccaaactcaa tttgaaactc 660
cgaagaaaaa ttcaccgaac actgaatctc agtttccaag gagcttcttc tacgaagagc 720
gcttcaattc cacgcagaac caccaagtca agccgggttcg tgactcggat tctcaattcc 780
tcgttcattc ccgaacgaat tttaaattcc gaagaaaacc gcaccgaaca ctgaatttca 840
gattctgaac aagtttcttc cgcgaaacag cacagcactt caatttcacg tggaacagag 900
acaaagggat tcgtgggttcg aattctcaat cgattttcaa attccgaaca gcgaacagta 960
cttcaatttc acgtcgaact agtcaaagcg attcaaactc atttcgcgaa ctcggtccgat 1020
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cgtagtcga tggcggactc cgacaacgac tccggcggcg cgcacaacgg cggcaagggg 1140
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MBI-0022CIP.ST25.txt

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aaggagaaga ggaagacgat caacggcgat gatctgctgt gggccatgac cacgctggga 1380
ttcgaggagt acgtggagcc tctcaagggt tatctgcata agtataggga gctggaaggg 1440
gagaaaaactg ctatgatggg aaggccacat gagagggatg agggttatgg tcatgcaact 1500
cctatgatga tcatgatggg gcatcagcag cagcagcatc agggacacgt gtatggatct 1560
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agaaacaccc cagctccagc ttgtaattgt tgcttgaaac ttcggtgttg agagaatata 1740
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<210> 52
 <211> 170
 <212> PRT
 <213> Glycine max

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 <223> G3473 GLYMA-28NOV01-CLUSTER33504_4 polypeptide

<400> 52

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Gly Ser Glu Met Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala
 20 25 30

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
 35 40 45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
 50 55 60

Ser Phe His Ser Pro Gly Gly Leu Ala Gly Glu Cys Gln Lys Glu Lys
 65 70 75 80

Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu
 85 90 95

Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Val Tyr Leu His Lys Tyr
 100 105 110

Arg Glu Leu Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His Glu

115

120

125

Arg Asp Glu Gly Tyr Gly His Ala Thr Pro Met Met Ile Met Met Gly
130 135 140

His Gln Gln Gln Gln His Gln Gly His Val Tyr Gly Ser Gly Thr Thr
145 150 155 160

Thr Gly Ser Ala Ser Ser Ala Arg Thr Arg
165 170

<210> 53
<211> 943
<212> DNA
<213> Oryza sativa

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<223> ORYSA-22JAN02-CLUSTER119015_1

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cggacgcggg gcacgacgag agcgggagcc cgccgaggag cggcgggggtg agggagcagg 180
acaggttcct gcccatcgcc aacatcagcc gcatcatgaa gaaggccgtc ccggcgaacg 240
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tcgtcaccag cgaggcgagc gacaaatgtc agaaggagaa gcgcaagacc atcaacgggg 360
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tctatttaca caagtacaga gagatggagg gtgatagtaa gctgtcctca aaggctggtg 480
atggttcagt aaagaaggat acaattgggtc cgcacagtgg cgctagtagc tcaagtgcgc 540
aagggatggg tggggcttac acccaaggga tgggttatat gcaacctcag tatcataatg 600
gggacaccta aagatgagga cagtgaataa tttcagtaac tgggtgtcctc tgtgagttat 660
tatccatctg ttaaggaaga acccacatta gggccatatt tattagtaga agactaaagc 720
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atgtaaatg cttcataagt ggtttaatgc ttgtttttgc ctgtatatc agagcaattt 840
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<210> 54
<211> 164
<212> PRT
<213> Oryza sativa

<200>

<223> ORYSA-22JAN02-CLUSTER119015_1 polypeptide

<400> 54

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Gly Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg
20 25 30

Ile Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala
35 40 45

Lys Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr
50 55 60

Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn
65 70 75 80

Gly Glu Asp Leu Leu Phe Ala Met Gly Thr Leu Gly Phe Glu Glu Tyr
85 90 95

Val Asp Pro Leu Lys Ile Tyr Leu His Lys Tyr Arg Glu Met Glu Gly
100 105 110

Asp Ser Lys Leu Ser Ser Lys Ala Gly Asp Gly Ser Val Lys Lys Asp
115 120 125

Thr Ile Gly Pro His Ser Gly Ala Ser Ser Ser Ser Ala Gln Gly Met
130 135 140

Val Gly Ala Tyr Thr Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His
145 150 155 160

Asn Gly Asp Thr

<210> 55

<211> 870

<212> DNA

<213> Zea mays

<200>

<223> Zm_S11418173

<400> 55

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cggcggggagc cacgagagcg ggagccccag gggagggcgga ggcggtggca gcgtcagggg 120

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tggcgacgat ctgctgtggg ccatggccac gctgggggtt gaagactaca ttgaaccctt 360
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tagcgatggc tcgattaaaa aggatgctct tggatcatgt ggagcaagta gtcagctgc 480
agaagggatg ggccaacagg gagcatacaa ccaaggaatg gggtatatgc aacctcagta 540
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acctgaggcg attttttttg tcttagttat ttactaagac accttgcggg gaccattaaa 660
gagtaaccaa tcgccctcaa taggtccgtt tttatctgcc agaactgatg aggtcgctca 720
ctaggagtaa gtcgcttccc tgggaacggg tgctcgctag caccgctctt gtatgtatat 780
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tcgggaggca taaatattgt gtaattgtgt 870
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<210> 56
 <211> 183
 <212> PRT
 <213> Zea mays

<200>
 <223> Zm_S11418173 polypeptide

<400> 56

Ala Gln Glu Glu Leu Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly
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Gly Gly Ser His Glu Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly
 20 25 30

Ser Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg
 35 40 45

Ile Met Lys Lys Ala Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala
 50 55 60

Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr
 65 70 75 80

Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn
 85 90 95

Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr

100 105 110

Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met Glu Gly
115 120 125

Asp Ser Lys Leu Thr Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp
130 135 140

Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Ala Glu Gly Met Gly
145 150 155 160

Gln Gln Gly Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr
165 170 175

His Asn Gly Asp Ile Ser Asn
180

<210> 57
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<212> DNA
<213> Zea mays

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<222> (712)..(712)
<223> n is a, c, g, or t

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<223> Zm_S11434692

<400> 57
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ccccgttgat tgtctttcgt ttctccttct ggcatttgct gctggcctcg ctggtcacga 600
atgatatgaa ctcgagagac cactcctgca ggggtctcctt agcgtccttg gcgatcttgc 660
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<210> 58
<211> 148
<212> PRT
<213> Zea mays

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<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid

<200>
<223> Zm_S11434692 polypeptide

<400> 58

Val Arg Glu Gln Asp Arg Phe Xaa Pro Ile Ala Asn Ile Ser Arg Ile
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Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys
20 25 30

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser
35 40 45

Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly
50 55 60

Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Val
65 70 75 80

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp
85 90 95

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala
100 105 110

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln
115 120 125

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His
130 135 140

Asn Gly Glu Thr
145

<210> 59
<211> 720
<212> DNA

<213> Triticum aestivum

<220>

<221> misc_feature

<222> (2)..(2)

<223> n is a, c, g, or t

<220>

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<222> (13)..(14)

<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> Ta_S45374

<400> 59

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gaattcggca ccagccacca ccttccctcc ctccacgagc cgtctatat aaggaggagg	180
gccggatgtc ggacgcgccc gcgagcccc cggcgggcgg cggcgggcga ggaggcggcg	240
gcagcgacga cggcgggcgg gcggcgggct tcggcgggct caggagcag gacagggtcc	300
tgcccatcgc caacatcagc cgcacatga agaaggccat cccggccaac ggcaagatcg	360
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gcgaggcgag cgacaagtgc cagaggaga agcgcaagac catcaacggc gacgacctgc	480
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agaagtacag agagacggag ggtgatagta agctagctgg aaagtctggt gaagtctctg	600
ttaaaaagga tgcacttggt cctcatggag gagcaagtgg cacaagtgcg caagggatgg	660
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<210> 60

<211> 179

<212> PRT

<213> Triticum aestivum

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<223> Xaa can be any naturally occurring amino acid

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 <223> Xaa can be any naturally occurring amino acid

<200>
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<400> 60

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Gly Gly Gly Ser Asp Asp Gly Gly Gly Gly Gly Gly Phe Gly Gly Val
 20 25 30

Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met
 35 40 45

Lys Lys Ala Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu
 50 55 60

Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu
 65 70 75 80

Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp
 85 90 95

Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Ile Glu
 100 105 110

Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Thr Glu Gly Asp Ser
 115 120 125

Lys Leu Ala Gly Lys Ser Gly Glu Val Ser Val Lys Lys Asp Ala Leu
 130 135 140

Gly Pro His Gly Gly Ala Ser Gly Thr Ser Ala Gln Gly Met Gly Gln
 145 150 155 160

Gln Val His Thr Ile Gln Glu Trp Xaa Ile Cys Asn Leu Ser Thr Ile
 165 170 175

Met Gly Xaa

<210> 61
 <211> 924
 <212> DNA

<213> Triticum aestivum

<220>

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<220>

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<223> n is a, c, g, or t

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<222> (536)..(536)

<223> n is a, c, g, or t

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<222> (546)..(546)

<223> n is a, c, g, or t

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<221> misc_feature

<222> (581)..(581)

<223> n is a, c, g, or t

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<222> (600)..(600)

<223> n is a, c, g, or t

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<222> (606)..(606)

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<222> (611)..(611)

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<222> (617)..(619)

<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (677)..(678)
<223> n is a, c, g, or t

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<222> (685)..(686)
<223> n is a, c, g, or t

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ctgcccacgc ccaatgtcag ccgatcatg aagaaggcgc tcccggccaa cgccaagatc	180
agcaaggacg ccaaggagac ggtgcaggag tgcgtctccg agttcatctc cttcatcacc	240
ggcgaggcct ccgacaagtg ccagcgcgag aagcgcaaga ccatnaacgg cgacgacctg	300
ctctgggcca tgaccacctt cggttcgag gactatgtcg acccgctcaa gcactacctn	360
cacaagttcc gcgagatcga gggcnagagg gccgcgcgcca catcaacatc aaccacgccc	420
gacatgccaa gaaacaacaa caacaatgcc cgccgggttac cccgacgccc cgggagggcat	480
gatgatgatg gggcagccca tgtaccggtt ngccggccgc accacaagga gcangnacc	540
aacatnaaaa ttgcaatggg gaggggagaa gcgggctttt nctattttgg aggcgggggn	600
gggtctctcg natcctnnng ggttttgacc gaaaaaanng ganacctttt cctttttctt	660
ttctttttctt tttggannct gaccnnaagg ggaggggntt ttcaaacttn tgttncttct	720
ttttgggtga aaacctnct tgnanctta aaattctttt cnnccccagg ggnggggaan	780
atntnttttt ttccccncgt tgnttgaaaa cctttttttt ttaaannttt ncgntntttc	840
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<211> 268

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 20 25 30

Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Ser Arg
 35 40 45

Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp Ala
 50 55 60

Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr
 65 70 75 80

Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Xaa Asn
 85 90 95

Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp Tyr
 100 105 110

Val Asp Pro Leu Lys His Tyr Xaa His Lys Phe Arg Glu Ile Glu Gly
 115 120 125

Xaa Arg Ala Ala Ala Thr Ser Thr Ser Thr Thr Pro Asp Met Pro Arg
 130 135 140

Asn Asn Asn Asn Asn Ala Arg Arg Leu Pro Arg Arg Pro Gly Arg His
 145 150 155 160

Asp Asp Asp Gly Ala Ala His Val Pro Val Xaa Arg Pro His His Lys
 165 170 175

Glu Xaa Xaa Pro Asn Xaa Lys Ile Ala Met Gly Arg Gly Glu Ala Gly
 180 185 190

Phe Xaa Tyr Phe Gly Gly Gly Xaa Gly Xaa Ser Xaa Ser Xaa Xaa Val
 195 200 205

Leu Thr Glu Lys Xaa Gly Xaa Leu Phe Leu Phe Leu Phe Phe Ser Phe

210		215		220
Trp Xaa Leu Thr Xaa Arg Gly Gly Xaa Phe Gln Thr Xaa Val Xaa Ser				
225		230	235	240
Phe Trp Val Lys Thr Xaa Leu Xaa Xaa Leu Lys Phe Phe Xaa Xaa Pro				
	245	250	255	
Gly Xaa Gly Xaa Xaa Xaa Phe Phe Pro Xaa Val Xaa				
	260	265		

<210> 63
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 <212> DNA
 <213> Lycopersicon esculentum

<200>
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tcccttcttc tccaacgtcc gatcttccag ttccctccat cccagtatg gcggatggtc	180
aagggttcgtc taggtcaccg gcgagtccaa acggaggtgg tagtcatgag agtgggtggg	240
accagagtcc gaggtctaata gtacgtgaac aggacagggtt tttaccaata gctaataatta	300
gtagaatcat gaagaaggca cttcctgcta atggaaaaat tgcgaaggat gctaaggaga	360
ctgttcagga atgtgtttct gagttcatca gcttcattac tagcgaggca agtgacaagt	420
gccagagaga gaaaaggaag actattaatg gtgacgattt gctatgggca atggcaactc	480
ttgggtttga agattatatt gaaccactca aggtgtatct tgctcgatac agagagatgg	540
agggaaacgtc aaaggctgct gatggctcta ctaaaagaga tgggatgcaa cctggtccta	600
attcacagct tgcacatcag ggttcatact cacaaggaat gaattatggg aattctcagg	660
gtcagcatat gatgggtccc atgcaaggaa ctgagtaaaa atccgatctt cgtcctgttt	720
gagaagacgg gtggagttga aaacatatta tatatataga tggttcttct gctgtaacct	780
ctgtaacatg gtttattaat tctagtgtc tctagtgtgt gccatgtcat atttaaagtt	840
tgtaaatga ggagatgttt taagaaatat tatagacatg attgtttgta gtaataatga	900
aaaccattac ctagtaaaaa aaaaaaaaaa aaaaa	935

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 <211> 176
 <212> PRT
 <213> Lycopersicon esculentum

<200>

<223> SGN-UNIGENE-46859 polypeptide

<400> 64

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1 5 10 15

Gly Gly Ser His Glu Ser Gly Gly Asp Gln Ser Pro Arg Ser Asn Val
20 25 30

Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met
35 40 45

Lys Lys Ala Leu Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu
50 55 60

Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu
65 70 75 80

Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp
85 90 95

Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu
100 105 110

Pro Leu Lys Val Tyr Leu Ala Arg Tyr Arg Glu Met Glu Gly Thr Ser
115 120 125

Lys Ala Ala Asp Gly Ser Thr Lys Arg Asp Gly Met Gln Pro Gly Pro
130 135 140

Asn Ser Gln Leu Ala His Gln Gly Ser Tyr Ser Gln Gly Met Asn Tyr
145 150 155 160

Gly Asn Ser Gln Gly Gln His Met Met Val Pro Met Gln Gly Thr Glu
165 170 175

<210> 65

<211> 1004

<212> DNA

<213> Lycopersicon esculentum

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<223> SGN-UNIGENE-47447

<400> 65

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taaaaatttt ctccattttc ttgttcttaa agcttggtgta ctatcatagg caaatacaag 120

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ggaacagaat ttaggcgatt tcgatggcgg attcggataa tgaatcagga ggacatagag 300
ataacagtaa cattgagagt tccctaagag aacaagacag gttccttccc atagcaaagt 360
taagcagaat catgaagaaa gctttaccag ctaacgcgaa aatctcaaaa gatgctaagg 420
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agtgtcaaag agaaaagaga aagacaatca atgggtgatga tctgttgtgg gcaatgacaa 540
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tggaagggca aaaaagtggg gtctctggag agaaggatca tagtggatca gtgggttatg 660
ttgaggacta ccatggcatg atgatgatgg ggagtcaaca tcatcaagga cgcggggatg 720
gcaccggtgt atacaatcat catacggggg agaatgctgc aggggttggg acaggagggt 780
cgcggtttcc tgacgttggg aggcaaaggt gaagctgtga catccgcgga ctacaaagat 840
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acagactttg tagtttgtat tctacagaga tgtaaattgg taaacatgtg tgtacattac 960
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<210> 66
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 <213> Lycopersicon esculentum

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 20 25 30

Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser
 35 40 45

Lys Asp Ala Lys Glu Val Val Gln Glu Cys Val Ser Glu Phe Ile Ser
 50 55 60

Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys
 65 70 75 80

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe

85

90

95

Glu Glu Tyr Ile Glu Pro Leu Lys Ile Tyr Leu Gln Arg Phe Arg Asp
100 105 110

Leu Glu Gly Gln Lys Ser Gly Val Ser Gly Glu Lys Asp His Ser Gly
115 120 125

Ser Val Gly Tyr Val Glu Asp Tyr His Gly Met Met Met Met Gly Ser
130 135 140

Gln His His Gln Gly Arg Gly Tyr Gly Thr Gly Val Tyr Asn His His
145 150 155 160

Thr Gly Glu Asn Ala Ala Gly Val Gly Thr Gly Gly Ser Arg Phe Pro
165 170 175

Asp Val Gly Arg Gln Arg
180

<210> 67
<211> 609
<212> DNA
<213> Arabidopsis thaliana

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<223> G1820

<400> 67
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attgagcaga tggaaaccgt ctcggatttc aaaaaccgtc agcttccatt ggctcgaatt 180
aagaagatca tgaaggctga tccagatgtg cacatggtct ccgcagaggc tccgatcatc 240
ttcgcaaagg cttgcgaaat gttcatcggt gatctcacga tgcggtcgtg gctcaaagcc 300
gaggagaaca aacgccacac gcttcagaaa tcggatatct ccaacgcagt ggctagctct 360
ttcacctacg atttccttct tgatgttgct cctaaggacg agtctatcgc caccgctgat 420
cctggctttt tggctatgcc acatcctgac ggtggaggag taccgcaata ttattatcca 480
ccgggagtgg tgatgggaac tcctatggtt ggtagtggaa tgtacgcgcc atcgcaggcg 540
tgggcagcag cggctggtga cggggaggat gatgctgagg ataatggagg aaacggcggc 600
ggaaattga 609

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<211> 202
<212> PRT

<213> Arabidopsis thaliana

<200>

<223> G1820 polypeptide

<400> 68

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20 25 30

Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser
35 40 45

Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
50 55 60

Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile
65 70 75 80

Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser
85 90 95

Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp
100 105 110

Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp
115 120 125

Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val
130 135 140

Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro
145 150 155 160

Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala
165 170 175

Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala
180 185 190

Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn
195 200

<210> 69

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<212> DNA

<213> Arabidopsis thaliana

<200>

<223> G1248

<400> 69

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caacagcaag aagaaagcat gatggtaaaa gaacaagaca ggctacttcc gatagcaaac      180
gtaggaagga tcatgaagaa catcctccca gcaaacgcaa aggtctctaa agaagccaaa      240
gagactatgc aagaatgtgt gtccgagttc attagcttcg tcacgggaga agcatccgat      300
aatgccaca aggagaagcg aaagaccgtt aatggagacg atatctgttg ggctatggct      360
aatctagggt ttgatgatta cgccgcccag ctcaagaagt acttacatcg ttaccgagtt      420
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<212> PRT

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<223> G1248 polypeptide

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20          25          30

Gly Leu Val Val Val Val Glu Asp Gln Gln Gln Glu Glu Ser Met Met
35          40          45

Val Lys Glu Gln Asp Arg Leu Leu Pro Ile Ala Asn Val Gly Arg Ile
50          55          60

Met Lys Asn Ile Leu Pro Ala Asn Ala Lys Val Ser Lys Glu Ala Lys
65          70          75          80

Glu Thr Met Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Gly
85          90          95

Glu Ala Ser Asp Lys Cys His Lys Glu Lys Arg Lys Thr Val Asn Gly
100         105         110

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Asp Asp Ile Cys Trp Ala Met Ala Asn Leu Gly Phe Asp Asp Tyr Ala
115 120 125

Ala Gln Leu Lys Lys Tyr Leu His Arg Tyr Arg Val Leu Glu Gly Glu
130 135 140

Lys Pro Asn His His Gly Lys Gly Gly Pro Lys Ser Ser Pro Asp Asn
145 150 155 160

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<211> 757
<212> DNA
<213> Arabidopsis thaliana

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<223> G1781

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ccaggaagcc cttcttcaaa gaccaacaac aacaacaaca acaacaaaga acaagaccgg 180
tttcttccca ttgcgaatgt cggaaggatc atgaaaaaag ttcttcccgg taacggtaag 240
atctcaaaag acgctaaaga aaccgttcaa gaatgtgtct cggagtcat tagtttcgtc 300
actggtgaag cttctgacaa gtgtcaaaga gaaagagga agaccatcaa tggagatgat 360
atcatttggg ctatcacaac tctcggttcc gaagactacg tggtccatt aaaggtctac 420
ctctgcaa atagagacac cgaaggagag aaagttaaca gcccacaaaca acaacaacaa 480
agacaacaac aacagcagat tcaacaacag aatcatcata attatcagtt tcaagaacaa 540
gacacaaaca ataacaacat gtcattgtact agttacatct ctcatcatca tccttctcca 600
ttctaccag tggatcatca accttttccc aatattgctt tctctcctaa atcattgcag 660
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ttgcttgagg gccgctctag gcgggaaaag cccgaat 757

<210> 72
<211> 215
<212> PRT
<213> Arabidopsis thaliana

<200>
<223> G1781 polypeptide

<400> 72

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20 25 30

Asn Asn Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Gly Arg
35 40 45

Ile Met Lys Lys Val Leu Pro Gly Asn Gly Lys Ile Ser Lys Asp Ala
50 55 60

Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr
65 70 75 80

Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn
85 90 95

Gly Asp Asp Ile Ile Trp Ala Ile Thr Thr Leu Gly Phe Glu Asp Tyr
100 105 110

Val Ala Pro Leu Lys Val Tyr Leu Cys Lys Tyr Arg Asp Thr Glu Gly
115 120 125

Glu Lys Val Asn Ser Pro Lys Gln Gln Gln Gln Arg Gln Gln Gln Gln
130 135 140

Gln Ile Gln Gln Gln Asn His His Asn Tyr Gln Phe Gln Glu Gln Asp
145 150 155 160

Gln Asn Asn Asn Asn Met Ser Cys Thr Ser Tyr Ile Ser His His His
165 170 175

Pro Ser Pro Phe Leu Pro Val Asp His Gln Pro Phe Pro Asn Ile Ala
180 185 190

Phe Ser Pro Lys Ser Leu Gln Lys Gln Phe Pro Gln Gln His Asp Asn
195 200 205

Asn Ile Asp Ser Ile His Trp
210 215

<210> 73
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<400> 73

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tcagccgcat catgaagaag gccgtcccgg cgaacggcaa gatcgccaag gacgccaagg      180
agaccctgca ggagtgcgtc tcggagttca tctccttcgt caccagcgag gcgagcgaca      240
aatgtcagaa ggagaagcgc aagaccatca acggggaaga tctcctcttt gcgatgggta      300
cgcttggttt tgaggagtac gttgatccgt tgaagatcta tttacacaag tacagagaga      360
tggaggggtga tagtaagctg tcctcaaagg ctggtgatgg ttcagtaaag aaggatacaa      420
ttggtccgca cagtggcgct agtagctcaa gtgcgcaagg gatgggtggg gcttacaccc      480
aagggatggg ttatatgcaa cctcagtatc ataatgggga cacctaaaga tgaggatagt      540
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acattagggc                                     610

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<210> 74
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 <212> PRT
 <213> Oryza sativa

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<400> 74

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Gly Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg
 20 25 30

Ile Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala
 35 40 45

Lys Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr
 50 55 60

Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn
 65 70 75 80

Gly Glu Asp Leu Leu Phe Ala Met Gly Thr Leu Gly Phe Glu Glu Tyr
 85 90 95

Val Asp Pro Leu Lys Ile Tyr Leu His Lys Tyr Arg Glu Met Glu Gly
 100 105 110

Asp Ser Lys Leu Ser Ser Lys Ala Gly Asp Gly Ser Val Lys Lys Asp

115

120

125

Thr Ile Gly Pro His Ser Gly Ala Ser Ser Ser Ser Ala Gln Gly Met
130 135 140

Val Gly Ala Tyr Thr Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His
145 150 155 160

Asn Gly Asp Thr

<210> 75
<211> 761
<212> DNA
<213> Oryza sativa

<200>
<223> G3398 AP005193

<400> 75
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gtcggcgagg gagcaggaca ggttcctgcc gatcgcgaaac gtgagcagga tcatgaagag 180
ggcgctcccg gcgaacgcca agatcagcaa ggacgccaag gagacggtgc aggagtgcgt 240
ctcggagttc atctccttca tcaccggcga ggcctccgac aagtgccagc gggagaagcg 300
caagaccatc aacggcgacg acctcctctg ggcatgacc acgctcggct tcgaggacta 360
catcgacccg ctcaagctct acctccacaa gttccgcgag ctcgagggcg agaaggccat 420
cggcgcgcgc ggcagcggcg gcggtggcgc cgcctcctcc ggcggctccg gctccggctc 480
cggctcgcac caccaccagg atgcttcccg gaacaatggc ggatacggca tgtacggcgg 540
cggcggcggc atgatcatga tgatgggaca gcctatgtac ggctcgccgc cggcgtcgtc 600
agctgggtac gcgcagccgc cgccgccccca ccaccaccac caccagatgg tgatgggagg 660
gaaagggtgcg tatggccatg gcggcggcgg cggcggcggg ccctccccgt cgtcgggata 720
cggccggcaa gacaggctat gagcttgctt tcttggttgg t 761

<210> 76
<211> 224
<212> PRT
<213> Oryza sativa

<200>
<223> G3398 AP005193 polypeptide

<400> 76

Met Pro Asp Ser Asp Asn Glu Ser Gly Gly Pro Ser Asn Ala Gly Glu

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Tyr Ala Ser Ala Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val
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Ser Arg Ile Met Lys Arg Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys
    35                40                45
Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
    50                55                60
Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
    65                70                75                80
Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu
    85                90                95
Asp Tyr Ile Asp Pro Leu Lys Leu Tyr Leu His Lys Phe Arg Glu Leu
    100                105                110
Glu Gly Glu Lys Ala Ile Gly Ala Ala Gly Ser Gly Gly Gly Gly Ala
    115                120                125
Ala Ser Ser Gly Gly Ser Gly Ser Gly Ser Gly Ser His His His Gln
    130                135                140
Asp Ala Ser Arg Asn Asn Gly Gly Tyr Gly Met Tyr Gly Gly Gly Gly
    145                150                155                160
Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Ser Pro Pro Ala
    165                170                175
Ser Ser Ala Gly Tyr Ala Gln Pro Pro Pro Pro His His His His His
    180                185                190
Gln Met Val Met Gly Gly Lys Gly Ala Tyr Gly His Gly Gly Gly Gly
    195                200                205
Gly Gly Gly Pro Ser Pro Ser Ser Gly Tyr Gly Arg Gln Asp Arg Leu
    210                215                220

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<210> 77
 <211> 856
 <212> DNA
 <213> Zea mays

<200>
 <223> G3434

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<400>. 77
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gcggcgagg cgtccgggag caggaccggt tcctgcccac cgccaacatc agccggatca      180
tgaagaaggc cgtccccggc aacggcaaga tcgccaagga cgctaaggag accctgcagg      240
agtgcgtctc cgagttcata tcattcgtga ccagcgaggc cagcgacaaa tgccagaagg      300
agaaacgaaa gacaatcaac ggggacgatt tgctctgggc gatggccact ttaggattcg      360
aggagtacgt cgagcctctc aagatttacc tacaaaagta caaagagatg gagggtgata      420
gcaagctgtc tacaaaggct ggcgagggct ctgtaaagaa ggatgcaatt agtccccatg      480
gtggcaccag tagctcaagt aatcagttgg ttcagcatgg agtctacaac caagggatgg      540
gctatatgca gccacagtac cacaatgggg aaacctata aagggttaat acagcagcaa      600
tttatgctag ggaagtctct gcattgctta ccatgtgtat tggcagaaaa caggaggcac      660
ttacaaaggg tgtaaatctc tgcgatggct gcctctcagg tgtaaattgg cttcggttta      720
gcgctgcttt tgtccgtata tttaggatga tttgactggt gctacttttg gcaacctttt      780
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tggtgattaa aaaaaa                                     856

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<210> 78
<211> 164
<212> PRT
<213> Zea mays

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<200>
<223> G3434 polypeptide

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<400> 78

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Met Ala Asp Asp Gly Gly Ser His Glu Gly Ser Gly Gly Gly Gly Gly
1          5          10          15

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Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile
          20          25          30

```

```

Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys
          35          40          45

```

```

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser
          50          55          60

```

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Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly
          65          70          75          80

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Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Val
85 90 95

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp
100 105 110

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala
115 120 125

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln
130 135 140

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His
145 150 155 160

Asn Gly Glu Thr

<210> 79
<211> 772
<212> DNA
<213> Glycine max

<200>
<223> G3472

<400> 79
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agggagcaag acaggttcct tccgatagcg aacgtgagca ggatcatgaa gaaggcgttg 180
ccggcgaacg cgaagatctc gaaggaggcg aaggagacgg tgcaggagtg cgtgtcggag 240
ttcatcagct tcataacagg agaagcgtcc gataagtgcc agaaggagaa gaggaagacg 300
atcaacggcg atgatctgct gtgggccatg accacgctgg gattcgagga gtacgtggag 360
cctctcaagg tttatctgca taagtatagg gagctggaag gggagaaaac tgctatgatg 420
ggaaggccac atgagagggg tgaggggttat ggtcatgcaa ctctatgat gatcatgatg 480
gggcatcaac agcagcagca tcagggaacac gtgtatggat ctggaactac tactggatca 540
gcatcttctg caagaactag ataacagggtt tatgcatgtg ttatctcatc tgtttaagct 600
tattaattga ttactataag gatggtgata ttgatttat attctgttg attttagaaa 660
cacaccgct ccagcttgta attgttgctt gaaacttcgt tgttgagaga atatagacat 720
tattgtggat ggtgatgtga catgcacaga atttttgtat tcttcttctt tt 772

<210> 80

<211> 171
<212> PRT
<213> Glycine max

<200>
<223> G3472 polypeptide

<400> 80

Met Ala Glu Ser Asp Asn Glu Ser Gly Gly His Thr Gly Asn Ala Ser
1 5 10 15

Gly Ser Asn Glu Phe Ser Gly Cys Arg Glu Gln Asp Arg Phe Leu Pro
20 25 30

Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala
35 40 45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
50 55 60

Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu
65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr
85 90 95

Leu Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Val Tyr Leu His Lys
100 105 110

Tyr Arg Glu Leu Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His
115 120 125

Glu Arg Asp Glu Gly Tyr Gly His Ala Thr Pro Met Met Ile Met Met
130 135 140

Gly His Gln Gln Gln Gln His Gln Gly His Val Tyr Gly Ser Gly Thr
145 150 155 160

Thr Thr Gly Ser Ala Ser Ser Ala Arg Thr Arg
165 170

<210> 81
<211> 1000
<212> DNA
<213> Glycine max

<200>
<223> G3474

<400> 81

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tccggttgca gggagcaaga caggttcctc ccaatagcaa acgtgagcag gatcatgaag      180
aaggcgttgc cggcgaacgc gaagatatcg aaggaggcga aggagacggt gcaggagtgc      240
gtgtcggagt tcatcagctt cataacagga gaggttccg ataagtgcc gaaggagaag      300
aggaagacga tcaacggcga cgatcttctc tgggccatga ctaccctggg cttcgaggac      360
tacgtggatc ctctcaagat ttacctgcac aagtataggg agatggaggg ggagaaaacc      420
gctatgatgg gaaggccaca tgagagggat gagggttatg gccatggcca tggatcatgca      480
actcctatga tgacgatgat gatggggcat cagccccagc accagcacca gcaccagcac      540
cagcaccagc accagggaca cgtgtatgga tctggatcag catcttctgc aagaactaga      600
tagcatgtgt catctgttta agcttaattg attttattat gaggatgata tgatataaga      660
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 <211> 181
 <212> PRT
 <213> Glycine max

<200>
 <223> G3474 polypeptide

<400> 82

Met Ala Glu Ser Asp Asn Glu Ser Gly Gly His Thr Gly Asn Ala Ser
 1 5 10 15

Gly Ser Asn Glu Leu Ser Gly Cys Arg Glu Gln Asp Arg Phe Leu Pro
 20 25 30

Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala
 35 40 45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
 50 55 60

Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu

65

70

75

80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr
85 90 95

Leu Gly Phe Glu Asp Tyr Val Asp Pro Leu Lys Ile Tyr Leu His Lys
100 105 110

Tyr Arg Glu Met Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His
115 120 125

Glu Arg Asp Glu Gly Tyr Gly His Gly His Gly His Ala Thr Pro Met
130 135 140

Met Thr Met Met Met Gly His Gln Pro Gln His Gln His Gln His Gln
145 150 155 160

His Gln His Gln His Gln Gly His Val Tyr Gly Ser Gly Ser Ala Ser
165 170 175

Ser Ala Arg Thr Arg
180

<210> 83
<211> 967
<212> DNA
<213> Glycine max

<200>
<223> G3477

<400> 83
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ttgtattgta atttgtaggg tttgtgagat gtcggatgca ccggcgagtc cgagtcacga 180
gagtggtagg gagcagagcc ctgcgggctc gttgtccggc gcggctagag agcaggaccg 240
gtaccttccc attgccaaca tcagccgcat catgaagaag gctctgcctc ccaatggcaa 300
gattgcgaag gatgcaaaaag acacaatgca agaatgcgtt tctgaattca tcagcttcat 360
taccagcgag gcgagtgaga aatgccagaa ggagaagaga aagacaatca atggagacga 420
tttactatgg gccatggcaa ctttaggggt tgaagactac attgagccgc ttaagggtga 480
cctgggctagg tacagagagg cggagggtga cactaaagga tctgctagaa gtggtgatgg 540
atctgctaca ccagatcaag ttggccttgc aggtcaaaaat tctcagcttg ttcacaggg 600
ttcgctgaac tatattgggt tgcaggtgca accacaacat ctggttatgc cttcaatgca 660

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 atatttg 967

<210> 84
 <211> 174
 <212> PRT
 <213> Glycine max

<200>
 <223> G3477 polypeptide

<400> 84

Met Ser Asp Ala Pro Ala Ser Pro Ser His Glu Ser Gly Gly Glu Gln
 1 5 10 15

Ser Pro Arg Gly Ser Leu Ser Gly Ala Ala Arg Glu Gln Asp Arg Tyr
 20 25 30

Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro
 35 40 45

Asn Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val
 50 55 60

Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln
 65 70 75 80

Lys Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met
 85 90 95

Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu
 100 105 110

Ala Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser
 115 120 125

Gly Asp Gly Ser Ala Thr Pro Asp Gln Val Gly Leu Ala Gly Gln Asn
 130 135 140

Ser Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val
 145 150 155 160

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Gln Pro Gln His Leu Val Met Pro Ser Met Gln Ser His Glu
165 170

<210> 85
<211> 864
<212> DNA
<213> Glycine max

<200>
<223> G3478

<400> 85
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ctccggcggc gcgcacaacg gcggcaaggg gagcgagatg tcgccgcggg agcaggaccg 180
gtttctcccg atcgcgaacg tgagccgcat catgaagaag gcgctgccgg cgaacgcgaa 240
gatctcgaag gacgcgaagg agacggtgca ggagtgcgtg tcagagttca tcagcttcat 300
caccggcggg gcctccgaca agtgccagcg cgagaagcgc aagacgatca acggcgacga 360
cctgctctgg gcgatgacca ctctgggctt cgaggactac gtggagcctc tcaaaggcta 420
cctccagcgc ttccgagaaa tggaaggaga gaagaccgtg gcggcgcgtg acaaggacgc 480
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cggtaggccc agataaatga gcctattatt attagtagta agttaaaaag aaaaatgtga 720
tatagtgggtg attagactga actagtttca acaaggctta atttgattgg taaagaatga 780
tgcatcacct cttcatctct attcgattct tattgataaa aaaaaaatta gagtgaacta 840
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<210> 86
<211> 191
<212> PRT
<213> Glycine max

<200>
<223> G3478 polypeptide

<400> 86

Met Ala Asp Ser Asp Asn Asp Ser Gly Gly Ala His Asn Gly Gly Lys
1 5 10 15

Gly Ser Glu Met Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala
20 25 30

MBI-0022CIP.ST25.txt

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
35 40 45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
50 55 60

Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg
65 70 75 80

Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly
85 90 95

Phe Glu Asp Tyr Val Glu Pro Leu Lys Gly Tyr Leu Gln Arg Phe Arg
100 105 110

Glu Met Glu Gly Glu Lys Thr Val Ala Ala Arg Asp Lys Asp Ala Pro
115 120 125

Pro Leu Thr Asn Ala Thr Asn Ser Ala Tyr Glu Ser Ala Asn Tyr Ala
130 135 140

Ala Ala Ala Ala Val Pro Gly Gly Ile Met Met His Gln Gly His Val
145 150 155 160

Tyr Gly Ser Ala Gly Phe His Gln Val Ala Gly Gly Ala Ile Lys Gly
165 170 175

Gly Pro Ala Tyr Pro Gly Pro Gly Ser Asn Ala Gly Arg Pro Arg
180 185 190

<210> 87
<211> 1231
<212> DNA
<213> Oryza sativa

<200>
<223> G3394 Cl26105_1

<400> 87
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gcagaagtac agagagatgg agggatgatag taaattaact gcaaaggctg gtgatggctc 660
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cccaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1231

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<210> 88
 <211> 185
 <212> PRT
 <213> Oryza sativa

<200>
 <223> G3394 C126105_1 polypeptide

<400> 88

Met Ala Asp Gly Pro Gly Ser Pro Gly Gly Gly Gly Gly Ser His Glu
 1 5 10 15

Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 20 25 30

Gly Gly Pro Leu Val Arg Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile
 35 40 45

Ser Arg Ile Met Lys Lys Ala Ile Pro Ala Asn Gly Lys Ile Ala Lys
 50 55 60

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
 65 70 75 80

Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr

85

90

95

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu
100 105 110

Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met
115 120 125

Glu Gly Asp Ser Lys Leu Thr Ala Lys Ala Gly Asp Gly Ser Val Lys
130 135 140

Lys Asp Val Leu Gly Ser His Gly Gly Ser Ser Ser Ser Ala Gln Gly
145 150 155 160

Met Gly Gln Gln Ala Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro
165 170 175

Gln Tyr His Asn Gly Asp Val Ser Asn
180 185

<210> 89
<211> 837
<212> DNA
<213> Oryza sativa

<200>
<223> G3396

<400> 89
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ttcgacggga cggagaacgg cggcggcggc ggcggaggcg gagtagggaa ggagcaggac 180
cggttcctgc cgatcgccaa catcggccgc atcatgcgcc gggccgtgcc ggagaacggc 240
aagatcgcca aggactccaa ggagtccgtc caggagtgcg tctccgagtt catcagcttc 300
atcaccagcg aagcaagcga caagtgcctc aaggagaagc gcaagaccat caatggggac 360
gacctgatct ggtcaatggg cacgctcgga ttcgaggact atgtcgagcc tctcaagctc 420
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gacgaggagt gtgatagcat ctaggaagga gaaccatcgt ttttagggaa agaacgctcc 600
agcatcctgt tatgttgtaa gcaggatgct tctaaagttc caataccttg ttaccacgaa 660
tgtagtcgt cgttcttttt gaaatgttct tgtgttagcc aggatgtcca aatttgttgt 720
aggttctagt tcagtcgtgt gttgtgtggt tgtgtctaac catatttggc cgtttccggc 780

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837

<210> 90
<211> 143
<212> PRT
<213> Oryza sativa

<200>
<223> G3396 polypeptide

<400> 90

Met Ser Glu Gly Phe Asp Gly Thr Glu Asn Gly Gly Gly Gly Gly Gly
1 5 10 15

Gly Gly Val Gly Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile
20 25 30

Gly Arg Ile Met Arg Arg Ala Val Pro Glu Asn Gly Lys Ile Ala Lys
35 40 45

Asp Ser Lys Glu Ser Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
50 55 60

Ile Thr Ser Glu Ala Ser Asp Lys Cys Leu Lys Glu Lys Arg Lys Thr
65 70 75 80

Ile Asn Gly Asp Asp Leu Ile Trp Ser Met Gly Thr Leu Gly Phe Glu
85 90 95

Asp Tyr Val Glu Pro Leu Lys Leu Tyr Leu Arg Leu Tyr Arg Glu Thr
100 105 110

Glu Gly Asp Thr Lys Gly Ser Arg Ala Ser Glu Leu Pro Val Lys Lys
115 120 125

Asp Val Val Leu Asn Gly Asp Pro Gly Ser Ser Phe Glu Gly Met
130 135 140

<210> 91
<211> 720
<212> DNA
<213> Oryza sativa

<200>
<223> G3397 AC120529

<400> 91
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ccgagcaact acgcgggagg ggagctgtcg tcgccgcggg agcaggacag gttcctgccg 120

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gcctccgaca agtgccagcg cgagaagcgc aagaccatca acggcgacga cctgctctgg 300
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gcctccacca cgccgccgca gcagcagcac accgccaatg ccgccggcgg ctacgccggg 480
tacgccgccc cgggagccgg ccccggcggc atgatgatga tgatggggca gcccatgtac 540
ggctcgccgc caccgccgcc acagcagcag cagcagcaac accaccacat ggcaatggga 600
ggaagaggcg gcttcgggtca tcatcccggc ggcggcggcg gcgggtcgtc gtcgtcgtcg 660
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<210> 92
<211> 219
<212> PRT
<213> Oryza sativa

<200>
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<400> 92

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20 25 30

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
35 40 45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
50 55 60

Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg
65 70 75 80

Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly
85 90 95

Phe Glu Asp Tyr Val Asp Pro Leu Lys His Tyr Leu His Lys Phe Arg
100 105 110

Glu Ile Glu Gly Glu Arg Ala Ala Ala Ser Thr Thr Gly Ala Gly Thr
115 120 125

Ser Ala Ala Ser Thr Thr Pro Pro Gln Gln Gln His Thr Ala Asn Ala
130 135 140

Ala Gly Gly Tyr Ala Gly Tyr Ala Ala Pro Gly Ala Gly Pro Gly Gly
145 150 155 160

Met Met Met Met Met Gly Gln Pro Met Tyr Gly Ser Pro Pro Pro Pro
165 170 175

Pro Gln Gln Gln Gln Gln Gln His His His Met Ala Met Gly Gly Arg
180 185 190

Gly Gly Phe Gly His His Pro Gly Gly Gly Gly Gly Gly Ser Ser Ser
195 200 205

Ser Ser Gly His Gly Arg Gln Asn Arg Gly Ala
210 215

<210> 93
<211> 1322
<212> DNA
<213> Zea mays

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<223> G3437

<400> 93
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tcgtaccgcg accaccagat ggccatgggc ggaaaagggtg gcgcctatgg ctacggcgga    1080
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gttggtgctga atggagccag tgatatggtt aagatagctc cataacctct cggtaaaaaa    1320
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<210> 94
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 <212> PRT
 <213> Zea mays

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 <223> G3437 polypeptide

<400> 94

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1 5 10 15

Val Gly Ser Pro Leu Ser Asp Asn Glu Ser Gly Ala Ala Ala Ala Ala
20 25 30

Gly Gly Gly Gly Cys Gly Ser Ser Val Gly Tyr Cys Gly Gly Gly Gly
35 40 45

Gly Glu Ser Pro Ala Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn
50 55 60

Val Ser Arg Ile Met Lys Arg Ser Leu Pro Ala Asn Ala Lys Ile Ser
65 70 75 80

Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser
85 90 95

Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys
100 105 110

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe
115 120 125

Glu Ala Tyr Val Ala Pro Leu Lys Ser Tyr Leu Asn Arg Tyr Arg Glu

130
 135
 140

Ala Glu Gly Glu Lys Ala Ala Val Leu Gly Gly Gly Ala Arg His Gly
 145 150 155 160

Asp Gly Ala Ala Arg Arg Thr Thr Pro Ala His Ser Pro Arg Asn Gly
 165 170 175

Ala Gly Gly Pro Val Gly Gly Tyr Gly Met Tyr Gly Gly Ala Gly Gly
 180 185 190

Gly Ser Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Gly Ser
 195 200 205

Pro Pro Ala Ala Ser Ser Gly Ser Tyr Pro His His Gln Met Ala Met
 210 215 220

Gly Gly Lys Gly Gly Ala Tyr Gly Tyr Gly Gly Gly Ser Ser Ser Ser
 225 230 235 240

Pro Ser Gly Leu Gly Arg
 245

<210> 95
 <211> 929
 <212> DNA
 <213> Arabidopsis thaliana

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 <223> CBF1

<400> 95
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 tttttctgaa atgtttggct ccgattacga gcctcaaggc ggagattatt gtccgacgtt 240
 ggccacgagt tgtccgaaga aaccggcggg ccgtaagaag tttcgtgaga ctcgtcacc 300
 aatttacaga ggagttcgtc aaagaaactc cggtaagtgg gtttctgaag tgagagagcc 360
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MBI-0022CIP.ST25.txt

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tgacgtgtcg ctttggagtt actaatattc gatagtcgtt tccatttttg tactatagtt 840
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gtagaaacga gtggaaaata attcaatac 929

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<210> 96
<211> 213
<212> PRT
<213> Arabidopsis thaliana

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<200>
<223> CBF1 polypeptide

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<400> 96

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Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
1           5           10           15

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Pro Gln Gly Gly Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys
          20           25           30

```

```

Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr
          35           40           45

```

```

Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg
          50           55           60

```

```

Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala
65           70           75           80

```

```

Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly
          85           90           95

```

```

Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile
          100          105          110

```

```

Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala
          115          120          125

```

```

Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Thr Asn His
          130          135          140

```

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Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu
145          150          155          160

```

```

Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met

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165

170

175

Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro
180 185 190

Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val
195 200 205

Ser Leu Trp Ser Tyr
210

<210> 97
<211> 803
<212> DNA
<213> Arabidopsis thaliana

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<223> CBF2

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ctccggtaag tgggtgtgtg agttgagaga gccaaacaag aaaacgagga tttggctcgg 240
gactttccaa accgctgaga tggcagctcg tgctcacgac gtcgccgcca tagctctccg 300
tggcagatct gcctgtctca atttcgctga ctgggcttgg cggctacgaa tcccgggaatc 360
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gatgtgtcat atgacgacgg atgctcatgg tcttgacatg gaggagacct tgggtggaggc 480
tatttatacg ccggaacaga gccaagatgc gttttatatg gatgaagagg cgatgttggg 540
gatgtctagt ttgttgata acatggccga agggatgctt ttaccgtcgc cgtcggttca 600
atggaactat aattttgatg tcgagggaga tgatgacgtg tccttatgga gctattaaaa 660
ttcgatTTTT atttccattt ttggtattat agctttttat acatttgatc cttttttaga 720
atggatcttc ttcttttttt ggttgtgaga aacgaatgta aatggtaaaa gttgttgtca 780
aatgcaaata tttttgagt cag 803

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<211> 207
<212> PRT
<213> Arabidopsis thaliana

<200>
<223> CBF2 polypeptide

<400> 98

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Met Phe Gly Ser Asp Tyr Glu Ser Pro Val Ser Ser Gly Gly Asp Tyr
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Ser Pro Lys Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly Arg Lys
20 25 30

Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg
35 40 45

Asn Ser Gly Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr
50 55 60

Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala
65 70 75 80

His Asp Val Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn
85 90 95

Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala
100 105 110

Lys Glu Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp
115 120 125

Glu Met Cys His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu
130 135 140

Thr Leu Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe
145 150 155 160

Tyr Met Asp Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn
165 170 175

Met Ala Glu Gly Met Leu Leu Pro Ser Pro Ser Val Gln Trp Asn Tyr
180 185 190

Asn Phe Asp Val Glu Gly Asp Asp Asp Val Ser Leu Trp Ser Tyr
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<210> 99
<211> 908
<212> DNA
<213> Arabidopsis thaliana

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<223> n is a, c, g, or t

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<223> CBF3

<400> 99

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aggcggatgat tatattccga cgcttgcgag cagctgcccc aagaaaccgg cgggtcgtaa 240
gaagtttcgt gagactcgtc acccaatata cagaggagtt cgtcggagaa actccggtaa 300
gtgggtttgt gaggttagag aaccaaacia gaaaacaagg atttggctcg gaacatttca 360
aaccgctgag atggcagctc gagctcacga cgctgcccgt ttagcccttc gtggccgatc 420
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ttatttccat ttttagtacg atacttttta ttttattatt attttttagat ctttttttag 840
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ttcagtat 908
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<210> 100

<211> 216

<212> PRT

<213> Arabidopsis thaliana

<200>

<223> CBF3 polypeptide

<400> 100

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Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
1          5          10          15
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Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
20          25          30
```

```
Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
35          40          45
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```
Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
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50		55		60
Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe				
65		70		80
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala				
	85		90	95
Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg				
	100		105	110
Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala				
	115		120	125
Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr				
	130		135	140
Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr				
	145		150	155
Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe				
	165		170	175
Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro				
	180		185	190
Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp				
	195		200	205
Asp Asp Val Ser Leu Trp Ser Tyr				
	210		215	
<210> 101				
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<213> Brassica napus				
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cgtgctcagc acgtcgtgc cctagccctc cgtggaagag gcgcctgcct caattatgcg				180
gactcggtt ggcgggtccg catcccgag acaacctgcc acaaggatat ccagaaggct				240
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 acgacgacgg atcatggcgt agacatggag gagacaatgg tggaggctgt ttttactggg 480
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 <211> 208
 <212> PRT
 <213> Brassica napus

<200>
 <223> bnCBF1 polypeptide

<400> 102

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Cys Glu Val Arg Glu Pro Asn Lys Lys Ser Arg Ile Trp Leu Gly Thr
 20 25 30

Phe Lys Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu
 35 40 45

Ala Leu Arg Gly Arg Gly Ala Cys Leu Asn Tyr Ala Asp Ser Ala Trp
 50 55 60

Arg Leu Arg Ile Pro Glu Thr Thr Cys His Lys Asp Ile Gln Lys Ala
 65 70 75 80

Ala Ala Glu Ala Ala Leu Ala Phe Glu Ala Glu Lys Ser Asp Val Thr
 85 90 95

Met Gln Asn Gly Gln Asn Met Glu Glu Thr Thr Ala Val Ala Ser Gln
 100 105 110

Ala Glu Val Asn Asp Thr Thr Thr Glu His Gly Met Asn Met Glu Glu
 115 120 125

Ala Thr Ala Val Ala Ser Gln Ala Glu Val Asn Asp Thr Thr Thr Asp
 130 135 140

His Gly Val Asp Met Glu Glu Thr Met Val Glu Ala Val Phe Thr Gly
 145 150 155 160

Glu Gln Ser Glu Gly Phe Asn Met Ala Lys Glu Ser Thr Val Glu Ala
165 170 175

Ala Val Val Thr Glu Glu Pro Ser Lys Gly Ser Tyr Met Asp Glu Glu
180 185 190

Trp Met Leu Glu Met Pro Thr Leu Leu Ala Asp Met Ala Glu Gly Met
195 200 205

<210> 103
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> Artificial sequence

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<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(18)
<223> n is a, c, g, or t

<200>
<223> Mol 368 reverse primer

<400> 103
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20

<210> 104
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> Artificial sequence

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
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<223> n is a, c, g, or t

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<220>
<221> misc_feature
<222> (18)..(18)
<223> n is a, c, g, or t

<200>
<223> Mol 378 forward primer

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